

revised.SUB.SEQUENCE.LST.0120  
SUBSTITUTE SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: PULST, STEFAN M.
- (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR  
ATAXIA-2 AND PRODUCTS RELATED THERETO
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
  - (B) STREET: 119 NORTH FOURTH STREET, SUITE 203
  - (C) CITY: MINNEAPOLIS
  - (D) STATE: MINNESOTA
  - (E) COUNTRY: 55401
  - (F) ZIP: 55401
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/981,998
  - (B) FILING DATE: 11-MAY-1998
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: WO 97/42314
  - (B) FILING DATE: 08-MAY-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/727,084
  - (B) FILING DATE: 08-OCT-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/022,207
  - (B) FILING DATE: 19-JUL-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/017,388
  - (B) FILING DATE: 08-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: MUETING, ANN M.
  - (B) REGISTRATION NUMBER: 33,977
  - (C) REFERENCE/DOCKET NUMBER: 232.00010120
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 612-305-1217
  - (B) TELEFAX: 612-305-1228

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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 516 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGTAGCAA CGGAAACGGC GGCGGCGCGT TTCGGCCCCG CTCCCGGCGG CTCCTTGGTC	60
TCGGCGGGCC TCCCCGCCCC TTCGTCGTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC	120
CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCC TGCGTCCCCG CCGCGTTCCG	180
GCGTCTCCTT GGCGCGCCCC GCTCCCGGCT GTCCCCGCCC GGCGTGCGAG CCGGTGTATG	240
GGCCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC	300
AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA	360
AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCCT	420
CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG	480
GGAGGCCCCG CCTGGGCAGG TGGGTGTCGG CACCCC	516

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 163..4101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACCCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG	60
GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG	120
CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCCCCTC CG ATG CGC TCA GCG	174
	Met Arg Ser Ala
	1
GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC	222
Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe	20
5 10 15	
GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG	270
Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg	35
25 30	
CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC	318

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Arg	Ser	Gly	Arg	Gly	Gly	Gly	Gly	Ala	Ala	Pro	Gly	Pro	Tyr	Pro	Ser		
			40					45					50				
GCC	GCC	CCT	CCC	CCG	CCC	GGC	CCC	GGC	CCC	CCT	CCC	TCC	CGG	CAG	AGC		366
Ala	Ala	Pro	Pro	Pro	Pro	Gly	Pro	Gly	Pro	Pro	Pro	Ser	Arg	Gln	Ser		
		55				60						65					
TCG	CCT	CCC	TCC	GCC	TCA	GAC	TGT	TTT	GGT	AGC	AAC	GGC	AAC	GGC	GGC		414
Ser	Pro	Pro	Ser	Ala	Ser	Asp	Cys	Phe	Gly	Ser	Asn	Gly	Asn	Gly	Gly		
	70					75					80						
GGC	GCG	TTT	CGG	CCC	GGC	TCC	CGG	CGG	CTC	CTT	GGT	CTC	GGC	GGG	CCT		462
Gly	Ala	Phe	Arg	Pro	Gly	Ser	Arg	Arg	Leu	Leu	Gly	Leu	Gly	Gly	Pro		
	85				90					95					100		
CCC	CGC	CCC	TTC	GTC	GTC	GTC	CTT	CTC	CCC	CTC	GCC	AGC	CCG	GGC	GCC		510
Pro	Arg	Pro	Phe	Val	Val	Val	Leu	Leu	Pro	Leu	Ala	Ser	Pro	Gly	Ala		
				105					110					115			
CCT	CCG	GCC	GCG	CCA	ACC	CGC	GCC	TCC	CCG	CTC	GGC	GCC	CGT	GCG	TCC		558
Pro	Pro	Ala	Ala	Pro	Thr	Arg	Ala	Ser	Pro	Leu	Gly	Ala	Arg	Ala	Ser		
			120					125					130				
CCG	CCG	CGT	TCC	GGC	GTC	TCC	TTG	GCG	CGC	CCG	GCT	CCC	GGC	TGT	CCC		606
Pro	Pro	Arg	Ser	Gly	Val	Ser	Leu	Ala	Arg	Pro	Ala	Pro	Gly	Cys	Pro		
		135					140					145					
CGC	CCG	GCG	TGC	GAG	CCG	GTG	TAT	GGG	CCC	CTC	ACC	ATG	TCG	CTG	AAG		654
Arg	Pro	Ala	Cys	Glu	Pro	Val	Tyr	Gly	Pro	Leu	Thr	Met	Ser	Leu	Lys		
	150					155					160						
CCC	CAG	CAG	CAG	CAG	CAG	CAG	CAG	CAG	CAA	CAG	CAG	CAG	CAG	CAA	CAG		702
Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln		
	165				170				175						180		
CAG	CAG	CAG	CAG	CAG	CAG	CAG	CCG	CCG	CCC	GCG	GCT	GCC	AAT	GTC	CGC		750
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Ala	Ala	Ala	Asn	Val	Arg		
				185					190					195			
AAG	CCC	GGC	GGC	AGC	GGC	CTT	CTA	GCG	TCG	CCC	GCC	GCC	GCG	CCT	TCG		798
Lys	Pro	Gly	Gly	Ser	Gly	Leu	Leu	Ala	Ser	Pro	Ala	Ala	Ala	Pro	Ser		
			200					205					210				
CCG	TCC	TCG	TCC	TCG	GTC	TCC	TCG	TCC	TCG	GCC	ACG	GCT	CCC	TCC	TCG		846
Pro	Ser	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ser	Ala	Thr	Ala	Pro	Ser	Ser		
		215				220						225					
GTG	GTC	GCG	GCG	ACC	TCC	GGC	GGC	GGG	AGG	CCC	GGC	CTG	GGC	AGA	GGT		894
Val	Val	Ala	Ala	Thr	Ser	Gly	Gly	Gly	Arg	Pro	Gly	Leu	Gly	Arg	Gly		
	230					235					240						
CGA	AAC	AGT	AAC	AAA	GGA	CTG	CCT	CAG	TCT	ACG	ATT	TCT	TTT	GAT	GGA		942
Arg	Asn	Ser	Asn	Lys	Gly	Leu	Pro	Gln	Ser	Thr	Ile	Ser	Phe	Asp	Gly		
	245				250					255					260		
ATC	TAT	GCA	AAT	ATG	AGG	ATG	GTT	CAT	ATA	CTT	ACA	TCA	GTT	GTT	GGC		990
Ile	Tyr	Ala	Asn	Met	Arg	Met	Val	His	Ile	Leu	Thr	Ser	Val	Val	Gly		
				265					270					275			
TCC	AAA	TGT	GAA	GTA	CAA	GTG	AAA	AAT	GGA	GGT	ATA	TAT	GAA	GGA	GTT		1038
Ser	Lys	Cys	Glu	Val	Gln	Val	Lys	Asn	Gly	Gly	Ile	Tyr	Glu	Gly	Val		

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280	285	290	
TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His 295 300 305			1086
GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu Ile Met 310 315 320			1134
GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys 325 330 335			1182
GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala 345 350 355			1230
ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro 360 365 370			1278
TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu 375 380 385			1326
AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn 390 395 400			1374
GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser 405 410 415 420			1422
TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg 425 430 435			1470
GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT GCC CAG Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln 440 445 450			1518
TAC AAA GCT CGA GTG GCC CTG GAA AAT GAT GAT AGG AGT GAG GAA GAA Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu 455 460 465			1566
AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG CAC AGC Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly His Ser 470 475 480			1614
ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA AAT AGA Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg 485 490 495 500			1662
GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT ATG GGC Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg Met Gly 505 510 515			1710
CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC ACT TCA Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His Thr Ser 520 525 530			1758

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GAT	TTC	AAC	CCG	AAT	TCT	GGT	TCA	GAC	CAA	AGA	GTA	GTT	AAT	GGA	GGT	1806
Asp	Phe	Asn	Pro	Asn	Ser	Gly	Ser	Asp	Gln	Arg	Val	Val	Asn	Gly	Gly	
		535					540					545				
GTT	CCC	TGG	CCA	TCG	CCT	TGC	CCA	TCT	CCT	TCC	TCT	CGC	CCA	CCT	TCT	1854
Val	Pro	Trp	Pro	Ser	Pro	Cys	Pro	Ser	Pro	Ser	Ser	Arg	Pro	Pro	Ser	
	550					555					560					
CGC	TAC	CAG	TCA	GGT	CCC	AAC	TCT	CTT	CCA	CCT	CGG	GCA	GCC	ACC	CCT	1902
Arg	Tyr	Gln	Ser	Gly	Pro	Asn	Ser	Leu	Pro	Pro	Arg	Ala	Ala	Thr	Pro	
565					570					575					580	
ACA	CGG	CCG	CCC	TCC	AGG	CCC	CCC	TCG	CGG	CCA	TCC	AGA	CCC	CCG	TCT	1950
Thr	Arg	Pro	Pro	Ser	Arg	Pro	Pro	Ser	Arg	Pro	Ser	Arg	Pro	Pro	Ser	
				585					590					595		
CAC	CCC	TCT	GCT	CAT	GGT	TCT	CCA	GCT	CCT	GTC	TCT	ACT	ATG	CCT	AAA	1998
His	Pro	Ser	Ala	His	Gly	Ser	Pro	Ala	Pro	Val	Ser	Thr	Met	Pro	Lys	
			600					605					610			
CGC	ATG	TCT	TCA	GAA	GGG	CCT	CCA	AGG	ATG	TCC	CCA	AAG	GCC	CAG	CGA	2046
Arg	Met	Ser	Ser	Glu	Gly	Pro	Pro	Arg	Met	Ser	Pro	Lys	Ala	Gln	Arg	
		615					620					625				
CAT	CCT	CGA	AAT	CAC	AGA	GTT	TCT	GCT	GGG	AGG	GGT	TCC	ATA	TCC	AGT	2094
His	Pro	Arg	Asn	His	Arg	Val	Ser	Ala	Gly	Arg	Gly	Ser	Ile	Ser	Ser	
	630					635					640					
GGC	CTA	GAA	TTT	GTA	TCC	CAC	AAC	CCA	CCC	AGT	GAA	GCA	GCT	ACT	CCT	2142
Gly	Leu	Glu	Phe	Val	Ser	His	Asn	Pro	Pro	Ser	Glu	Ala	Ala	Thr	Pro	
645					650					655					660	
CCA	GTA	GCA	AGG	ACC	AGT	CCC	TCG	GGG	GGA	ACG	TGG	TCA	TCA	GTG	GTC	2190
Pro	Val	Ala	Arg	Thr	Ser	Pro	Ser	Gly	Gly	Thr	Trp	Ser	Ser	Val	Val	
				665					670					675		
AGT	GGG	GTT	CCA	AGA	TTA	TCC	CCT	AAA	ACT	CAT	AGA	CCC	AGG	TCT	CCC	2238
Ser	Gly	Val	Pro	Arg	Leu	Ser	Pro	Lys	Thr	His	Arg	Pro	Arg	Ser	Pro	
			680					685					690			
AGA	CAG	AAC	AGT	ATT	GGA	AAT	ACC	CCC	AGT	GGG	CCA	GTT	CTT	GCT	TCT	2286
Arg	Gln	Asn	Ser	Ile	Gly	Asn	Thr	Pro	Ser	Gly	Pro	Val	Leu	Ala	Ser	
		695					700					705				
CCC	CAA	GCT	GGT	ATT	ATT	CCA	ACT	GAA	GCT	GTT	GCC	ATG	CCT	ATT	CCA	2334
Pro	Gln	Ala	Gly	Ile	Ile	Pro	Thr	Glu	Ala	Val	Ala	Met	Pro	Ile	Pro	
	710					715					720					
GCT	GCA	TCT	CCT	ACG	CCT	GCT	AGT	CCT	GCA	TCG	AAC	AGA	GCT	GTT	ACC	2382
Ala	Ala	Ser	Pro	Thr	Pro	Ala	Ser	Pro	Ala	Ser	Asn	Arg	Ala	Val	Thr	
725					730					735					740	
CCT	TCT	AGT	GAG	GCT	AAA	GAT	TCC	AGG	CTT	CAA	GAT	CAG	AGG	CAG	AAC	2430
Pro	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Arg	Leu	Gln	Asp	Gln	Arg	Gln	Asn	
				745					750					755		
TCT	CCT	GCA	GGG	AAT	AAA	GAA	AAT	ATT	AAA	CCC	AAT	GAA	ACA	TCA	CCT	2478
Ser	Pro	Ala	Gly	Asn	Lys	Glu	Asn	Ile	Lys	Pro	Asn	Glu	Thr	Ser	Pro	
			760					765					770			

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AGC Ser	TTC Phe	TCA Ser 775	AAA Lys	GCT Ala	GAA Glu	AAC Asn	AAA Lys 780	GGT Gly	ATA Ile	TCA Ser	CCA Pro	GTT Val 785	GTT Val	TCT Ser	GAA Glu	2526
CAT His	AGA Arg 790	AAA Lys	CAG Gln	ATT Ile	GAT Asp	GAT Asp 795	TTA Leu	AAG Lys	AAA Lys	TTT Phe	AAG Lys 800	AAT Asn	GAT Asp	TTT Phe	AGG Arg	2574
TTA Leu 805	CAG Gln	CCA Pro	AGT Ser	TCT Ser	ACT Thr 810	TCT Ser	GAA Glu	TCT Ser	ATG Met	GAT Asp 815	CAA Gln	CTA Leu	CTA Leu	AAC Asn	AAA Lys 820	2622
AAT Asn	AGA Arg	GAG Glu	GGA Gly	GAA Glu 825	AAA Lys	TCA Ser	AGA Arg	GAT Asp	TTG Leu 830	ATC Ile	AAA Lys	GAC Asp	AAA Lys	ATT Ile 835	GAA Glu	2670
CCA Pro	AGT Ser	GCT Ala	AAG Lys 840	GAT Asp	TCT Ser	TTC Phe	ATT Ile	GAA Glu 845	AAT Asn	AGC Ser	AGC Ser	AGC Ser	AAC Asn 850	TGT Cys	ACC Thr	2718
AGT Ser	GGC Gly	AGC Ser 855	AGC Ser	AAG Lys	CCG Pro	AAT Asn	AGC Ser 860	CCC Pro	AGC Ser	ATT Ile	TCC Ser	CCT Pro 865	TCA Ser	ATA Ile	CTT Leu	2766
AGT Ser	AAC Asn 870	ACG Thr	GAG Glu	CAC His	AAG Lys	AGG Arg 875	GGA Gly	CCT Pro	GAG Glu	GTC Val	ACT Thr 880	TCC Ser	CAA Gln	GGG Gly	GTT Val	2814
CAG Gln 885	ACT Thr	TCC Ser	AGC Ser	CCA Pro	GCA Ala 890	TGT Cys	AAA Lys	CAA Gln	GAG Glu	AAA Lys 895	GAC Asp	GAT Asp	AAG Lys	GAA Glu	GAG Glu 900	2862
AAG Lys	AAA Lys	GAC Asp	GCA Ala	GCT Ala 905	GAG Glu	CAA Gln	GTT Val	AGG Arg	AAA Lys 910	TCA Ser	ACA Thr	TTG Leu	AAT Asn	CCC Pro 915	AAT Asn	2910
GCA Ala	AAG Lys	GAG Glu	TTC Phe 920	AAC Asn	CCA Pro	CGT Arg	TCC Ser	TTC Phe 925	TCT Ser	CAG Gln	CCA Pro	AAG Lys	CCT Pro 930	TCT Ser	ACT Thr	2958
ACC Thr	CCA Pro	ACT Thr 935	TCA Ser	CCT Pro	CGG Arg	CCT Pro	CAA Gln 940	GCA Ala	CAA Gln	CCT Pro	AGC Ser	CCA Pro 945	TCT Ser	ATG Met	GTG Val	3006
GGT Gly	CAT His 950	CAA Gln	CAG Gln	CCA Pro	ACT Thr	CCA Pro 955	GTT Val	TAT Tyr	ACT Thr	CAG Gln	CCT Pro 960	GTT Val	TGT Cys	TTT Phe	GCA Ala	3054
CCA Pro 965	AAT Asn	ATG Met	ATG Met	TAT Tyr	CCA Pro 970	GTC Val	CCA Pro	GTG Val	AGC Ser	CCA Pro 975	GGC Gly	GTG Val	CAA Gln	CCT Pro	TTA Leu 980	3102
TAC Tyr	CCA Pro	ATA Ile	CCT Pro	ATG Met 985	ACG Thr	CCC Pro	ATG Met	CCA Pro	GTG Val 990	AAT Asn	CAA Gln	GCC Ala	AAG Lys	ACA Thr 995	TAT Tyr	3150
AGA Arg	GCA Ala	GTA Val	CCA Pro 1000	AAT Asn	ATG Met	CCC Pro	CAA Gln	CAG Gln 1005	CGG Arg	CAA Gln	GAC Asp	CAG Gln	CAT His 1010	CAT His	CAG Gln	3198
AGT	GCC	ATG	ATG	CAC	CCA	GCG	TCA	GCA	GCG	GGC	CCA	CCG	ATT	GCA	GCC	3246

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Ser Ala Met Met His Pro Ala	Ser Ala Ala Gly Pro Pro Ile Ala Ala	
1015	1020 1025	
ACC CCA CCA GCT TAC TCC ACG CAA TAT GTT GCC TAC AGT CCT CAG CAG		3294
Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr Ser Pro Gln Gln	1030 1035 1040	
TTC CCA AAT CAG CCC CTT GTT CAG CAT GTG CCA CAT TAT CAG TCT CAG		3342
Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His Tyr Gln Ser Gln	1045 1050 1055 1060	
CAT CCT CAT GTC TAT AGT CCT GTA ATA CAG GGT AAT GCT AGA ATG ATG		3390
His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn Ala Arg Met Met	1065 1070 1075	
GCA CCA CCA ACA CAC GCC CAG CCT GGT TTA GTA TCT TCT TCA GCA ACT		3438
Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser Ser Ser Ala Thr	1080 1085 1090	
CAG TAC GGG GCT CAT GAG CAG ACG CAT GCG ATG TAT GCA TGT CCC AAA		3486
Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr Ala Cys Pro Lys	1095 1100 1105	
TTA CCA TAC AAC AAG GAG ACA AGC CCT TCT TTC TAC TTT GCC ATT TCC		3534
Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr Phe Ala Ile Ser	1110 1115 1120	
ACG GGC TCC CTT GCT CAG CAG TAT GCG CAC CCT AAC GCT ACC CTG CAC		3582
Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn Ala Thr Leu His	1125 1130 1135 1140	
CCA CAT ACT CCA CAC CCT CAG CCT TCA GCT ACC CCC ACT GGA CAG CAG		3630
Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly Gln Gln	1145 1150 1155	
CAA AGC CAA CAT GGT GGA AGT CAT CCT GCA CCC AGT CCT GTT CAG CAC		3678
Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser Pro Val Gln His	1160 1165 1170	
CAT CAG CAC CAG GCC GCC CAG GCT CTC CAT CTG GCC AGT CCA CAG CAG		3726
His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala Ser Pro Gln Gln	1175 1180 1185	
CAG TCA GCC ATT TAC CAC GCG GGG CTT GCG CCA ACT CCA CCC TCC ATG		3774
Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr Pro Pro Ser Met	1190 1195 1200	
ACA CCT GCC TCC AAC ACG CAG TCG CCA CAG AAT AGT TTC CCA GCA GCA		3822
Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser Phe Pro Ala Ala	1205 1210 1215 1220	
CAA CAG ACT GTC TTT ACG ATC CAT CCT TCT CAC GTT CAG CCG GCG TAT		3870
Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln Pro Ala Tyr	1225 1230 1235	
ACC AAC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA CAG TCA		3918
Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala His Val Gln Ser	1240 1245 1250	
GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG CTA ATG		3966
Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met Leu Met		

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1260 1265

1255	ACG ACA CAG CCA CCC GGC GGT CCC CAG GCC GCC CTC GCT CAA AGT GCA	4014
	Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu Ala Gln Ser Ala	
	1270 1275 1280	
	CTA CAG CCC ATT CCA GTC TCG ACA ACA GCG CAT TTC CCC TAT ATG ACG	4062
	Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr Met Thr	
	1285 1290 1295 1300	
	CAC CCT TCA GTA CAA GCC CAC CAC CAA CAG CAG TTG TAA GGCTGCCCTG	4111
	His Pro Ser Val Gln Ala His His Gln Gln Gln Leu *	
	1305 1310	
	GAGGAACCGA AAGGCCAAAT TCCCTCCTCC CTTCTACTGC TTCTACCAAC TGGGAAGCACA	4171
	GAAAACTAGA ATTTCAATTA TTTTGTITTT AAAATATATA TGTTGATTTC TTGTAACATC	4231
	CAATAGGAAT GCTAACAGTT CACTTGCACT GGAAGATACT TGGACCGAGT AGAGGCATTT	4291
	AGGAACTTGG GGGCTATTCC ATAATTCCAT ATGCTGTTTC AGAGTCCCGC AGGTACCCCA	4351
	GCTCTGCTTG CCGAACTGG AAGTTATTTA TTTTITAATA ACCCTTGAAA GTCATGAACA	4411
	CATCAGCTAG CAAAAGAAGT AACAAGAGTG ATTCTTGCTG CTATTACTGC TAAAAA	4471
	AAAAA	4481

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Arg Ser Ala Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu  
1 5 10 15

Ser Arg Arg Phe Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln  
20 25 30

Arg Pro Ala Arg Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly  
35 40 45

Pro Tyr Pro Ser Ala Ala Pro Pro Pro Gly Pro Gly Pro Pro Pro  
50 55 60

Ser Arg Gln Ser Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn  
65 70 75 80

Gly Asn Gly Gly Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly  
85 90 95

Leu Gly Gly Pro Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala  
100 105 110

Ser Pro Gly Ala Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly  
115 120 125



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Ala Arg Ala Ser Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala  
130 135 140  
Pro Gly Cys Pro Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr  
145 150 155 160  
Met Ser Leu Lys Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln  
165 170 175  
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala  
180 185 190  
Ala Asn Val Arg Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala  
195 200 205  
Ala Ala Pro Ser Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr  
210 215 220  
Ala Pro Ser Ser Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly  
225 230 235 240  
Leu Gly Arg Gly Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile  
245 250 255  
Ser Phe Asp Gly Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr  
260 265 270  
Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile  
275 280 285  
Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu  
290 295 300  
Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg  
305 310 315 320  
Glu Glu Ile Met Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val  
325 330 335  
Val Gln Phe Lys Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe  
340 345 350  
Thr Asp Ser Ala Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys  
355 360 365  
Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu  
370 375 380  
Glu Ala Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met  
385 390 395 400  
Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser  
405 410 415  
Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu  
420 425 430  
Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu  
435 440 445  
Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg  
450 455 460

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Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg  
465 470 475 480

Glu Gly His Ser Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly  
485 490 495

Gln Arg Asn Arg Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser  
500 505 510

Pro Arg Met Gly Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr  
515 520 525

Ser His Thr Ser Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val  
530 535 540

Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser  
545 550 555 560

Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg  
565 570 575

Ala Ala Thr Pro Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser  
580 585 590

Arg Pro Pro Ser His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser  
595 600 605

Thr Met Pro Lys Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro  
610 615 620

Lys Ala Gln Arg His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly  
625 630 635 640

Ser Ile Ser Ser Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu  
645 650 655

Ala Ala Thr Pro Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp  
660 665 670

Ser Ser Val Val Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg  
675 680 685

Pro Arg Ser Pro Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro  
690 695 700

Val Leu Ala Ser Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala  
705 710 715 720

Met Pro Ile Pro Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn  
725 730 735

Arg Ala Val Thr Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp  
740 745 750

Gln Arg Gln Asn Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn  
755 760 765

Glu Thr Ser Pro Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro  
770 775 780

Val Val Ser Glu His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys

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785 790 795 800  
 Asn Asp Phe Arg Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln  
 805 810 815  
 Leu Leu Asn Lys Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys  
 820 825 830  
 Asp Lys Ile Glu Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser  
 835 840 845  
 Ser Asn Cys Thr Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser  
 850 855 860  
 Pro Ser Ile Leu Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr  
 865 870 875 880  
 Ser Gln Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp  
 885 890 895  
 Asp Lys Glu Glu Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr  
 900 905 910  
 Leu Asn Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro  
 915 920 925  
 Lys Pro Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser  
 930 935 940  
 Pro Ser Met Val Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro  
 945 950 955 960  
 Val Cys Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly  
 965 970 975  
 Val Gln Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln  
 980 985 990  
 Ala Lys Thr Tyr Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp  
 995 1000 1005  
 Gln His His Gln Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro  
 1010 1015 1020  
 Pro Ile Ala Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr  
 1025 1030 1035 1040  
 Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His  
 1045 1050 1055  
 Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn  
 1060 1065 1070  
 Ala Arg Met Met Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser  
 1075 1080 1085  
 Ser Ser Ala Thr Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr  
 1090 1095 1100  
 Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr  
 1105 1110 1115 1120

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Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn  
1125 1130 1135

Ala Thr Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro  
1140 1145 1150

Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser  
1155 1160 1165

Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala  
1170 1175 1180

Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr  
1185 1190 1195 1200

Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser  
1205 1210 1215

Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val  
1220 1225 1230

Gln Pro Ala Tyr Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala  
1235 1240 1245

His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro  
1250 1255 1260

Met Met Leu Met Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu  
1265 1270 1275 1280

Ala Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe  
1285 1290 1295

Pro Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu  
1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3798 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 50..3457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCACGAGGT CCCC GCCCGG CGTGCGAGCC GGTGTATGGG CCGCTCACC ATG TCG 55  
Met Ser  
1

CTG AAG CCG CAG CCG CAG CCG CCC GCG CCC GCC ACT GGC CGC AAG CCC 103

Leu Lys Pro Gln Pro Gln Pro Pro Ala Pro Ala Thr Gly Arg Lys Pro  
5 10 15

GTG ACC TCG GCT TCC GTG GTG CCG GCC CCG GCC GCG CCG GTG GCG TCT  
Val Thr Ser Ala Ser Val Val Pro Ala Pro Ala Ala Pro Val Ala Ser  
35 40 45 50 199

AAC AGT AGC AAA GGA CTG CCT CAG CCT ACG ATT TCT TTT GAT GGA ATC 295  
Asn Ser Ser Lys Gly Leu Pro Gln Pro Thr Ile Ser Phe Asp Gly Ile  
70 75 80

AAA TGT GAA GTA CAA GTG AAA AAC GGA GGC ATA TAT GAA GGA GTT TTT 391  
Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val Phe  
100 105 110

AAA AGT ACA GAA TCC AGT TCG GGG CCA AAA CGT GAA GAA ATA ATG GAG 487  
Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu Ile Met Glu  
135 140 145

ACA GAC TCC AGT TAT GCA CGG AGA GAT GCT TTT ACT GAC TCT GCT CTC 583  
Thr Asp Ser Ser Tyr Ala Arg Arg Asp Ala Phe Thr Asp Ser Ala Leu  
165 170 175

GAT GCA GGG GAG CTC ACG GCC AGC GAG GAG CTG GAG CTG GAG AAT GAT  
Asp Ala Gly Glu Leu Thr Ala Ser Glu Glu Leu Glu Leu Glu Asn Asp  
195 200 205 210 679

AAT TAT GGT GTG GTG TCC ACA TAT GAT AGC AGT TTA TCT TCA TAT ACG 775  
Asn Tyr Gly Val Val Ser Thr Gln Ser Ser Tyr Thr

Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg Glu Ala  
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250 255

245	AGG GCA AAC CAG TTA GCA GAA GAA ATT GAA TCC AGT GCT CAG TAC AAA Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln Tyr Lys 260 265 270	871
	GCT CGT GTC GCC CTT GAG AAT GAT GAC CGG AGT GAG GAA GAA AAA TAC Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu Lys Tyr 275 280 285 290	919
	ACA GCA GTC CAG AGA AAC TGC AGT GAC CGG GAG GGG CAT GGC CCC AAC Thr Ala Val Gln Arg Asn Cys Ser Asp Arg Glu Gly His Gly Pro Asn 295 300 305	967
	ACT AGG GAC AAT AAA TAT ATT CCT CCT GGA CAA AGA AAC AGA GAA GTC Thr Arg Asp Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg Glu Val 310 315 320	1015
	CTA TCC TGG GGA AGT GGG AGA CAG AGC TCA CCA CGG ATG GGC CAG CCT Leu Ser Trp Gly Ser Gly Arg Gln Ser Ser Pro Arg Met Gly Gln Pro 325 330 335	1063
	GGG CCA GGC TCC ATG CCG TCA AGA GCT GCT TCT CAC ACT TCA GAT TTC Gly Pro Gly Ser Met Pro Ser Arg Ala Ala Ser His Thr Ser Asp Phe 340 345 350	1111
	AAC CCG AAC GCT GGC TCA GAC CAA AGA GTA GTT AAT GGA GGT GTT CCC Asn Pro Asn Ala Gly Ser Asp Gln Arg Val Val Asn Gly Gly Val Pro 355 360 365 370	1159
	TGG CCA TCG CCT TGC CCA TCT CAT TCC TCT CGC CCA CCT TCT CGC TAC Trp Pro Ser Pro Cys Pro Ser His Ser Ser Arg Pro Pro Ser Arg Tyr 375 380 385	1207
	CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CAT ACA CGG Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr His Thr Arg 390 395 400	1255
	CCG CCC TCC AGG CCC CCC TCG AGG CCA TCC AGA CCC CCG TCT CAC CCC Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser His Pro 405 410 415	1303
	TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA CGC ATG Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys Arg Met 420 425 430	1351
	TCT TCA GAA GGA CCC CCA AGG ATG TCT CCA AAG GCA CAG CGC CAC CCT Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg His Pro 435 440 445 450	1399
	CGG AAT CAC AGA GTC TCT GCT GGG AGA GGC TCC ATG TCT AGT GGC CTA Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Met Ser Ser Gly Leu 455 460 465	1447
	GAA TTT GTA TCC CAC AAT CCC CCA AGT GAA GCA GCT GCT CCT CCA GTG Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Ala Pro Pro Val 470 475 480	1495
	GCA AGG ACC AGT CCT GCA GGG GGA ACG TGG TCC TCA GTG GTC AGT GGG Ala Arg Thr Ser Pro Ala Gly Gly Thr Trp Ser Ser Val Val Ser Gly 485 490 495	1543

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GTT CCA AGG TTA TCT CCC AAA ACT CAC AGA CCC AGG TCT CCC AGG CAG Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro Arg Gln 500 505 510	1591
AGC AGC ATT GGA AAC TCT CCC AGC GGG CCT GTG CTT GCT TCT CCC CAA Ser Ser Ile Gly Asn Ser Pro Ser Gly Pro Val Leu Ala Ser Pro Gln 515 520 525 530	1639
GCT GGC ATC ATC CCT GCA GAA GCC GTT TCC ATG CCT GTT CCC GCC GCA Ala Gly Ile Ile Pro Ala Glu Ala Val Ser Met Pro Val Pro Ala Ala 535 540 545	1687
TCT CCG ACT CCT GCC AGC CCT GCA TCC AAC AGA GCA CTG ACC CCA TCT Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Leu Thr Pro Ser 550 555 560	1735
ATT GAG GCA AAA GAT TCC AGG CTT CAA GAT CAG AGG CAG AAC TCT CCT Ile Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn Ser Pro 565 570 575	1783
GCA GGG AGT AAA GAA AAT GTT AAA GCA AGT GAA ACA TCA CCT AGC TTT Ala Gly Ser Lys Glu Asn Val Lys Ala Ser Glu Thr Ser Pro Ser Phe 580 585 590	1831
TCA AAA GCT GAC AAC AAA GGT ATG TCA CCA GTT GTT TCT GAA CAC AGA Ser Lys Ala Asp Asn Lys Gly Met Ser Pro Val Val Ser Glu His Arg 595 600 605 610	1879
AAA CAG ATT GAT GAC TTA AAG AAG TTT AAG AAT GAT TTT AGG TTA CAG Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg Leu Gln 615 620 625	1927
CCA AGC TCT ACA TCT GAA TCT ATG GAT CAA CTA CTA AGC AAA AAT AGA Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Ser Lys Asn Arg 630 635 640	1975
GAA GGA GAA AAG TCA CGA GAT TTG ATT AAA GAT AAA ACG GAA GCA AGT Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Thr Thr Glu Ala Ser 645 650 655	2023
GCT AAG GAT AGT TTC ATT GAC AGC AGC AGC AGC AGC AGC AAC TGT ACC Ala Lys Asp Ser Phe Ile Asp Ser Ser Ser Ser Ser Ser Asn Cys Thr 660 665 670	2071
AGT GGC AGC AGC AAG ACC AAC AGC CCT AGC ATC TCC CCT TCC ATG CTT Ser Gly Ser Ser Lys Thr Asn Ser Pro Ser Ile Ser Pro Ser Met Leu 675 680 685 690	2119
AGT AAT GCA GAG CAC AAG AGG GGG CCT GAG GTC ACA TCC CAA GGG GTG Ser Asn Ala Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln Gly Val 695 700 705	2167
CAG ACT TCC AGC CCA GCC TGC AAA CAA GAG AAG GAT GAC AGA GAA GAG Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Arg Glu Glu 710 715 720	2215
AAG AAA GAC ACA ACA GAG CAG GTT AGG AAA TCG ACA TTG AAT CCC AAT Lys Lys Asp Thr Thr Glu Gln Val Arg Lys Ser Thr Leu Asn Pro Asn 725 730 735	2263

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GCA AAG GAG TTC AAC CCT CGT TCT TTC TCT CAG CCA AAG CCT TCT ACT Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro Ser Thr 740 745 750	2311
ACC CCA ACG TCA CCT CGG CCT CAA GCA CAA CCC AGC CCA TCT ATG GTG Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser Met Val 755 760 765 770	2359
GGT CAT CAG CAG CCA GCT CCA GTG TAC ACT CAG CCT GTG TGC TTC GCA Gly His Gln Gln Pro Ala Pro Val Tyr Thr Gln Pro Val Cys Phe Ala 775 780 785	2407
CCC AAT ATG ATG TAT CCC GTC CCA GTG AGC CCG GGC GTA CAA CCT TTA Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln Pro Leu 790 795 800	2455
TAC CCA ATA CCT ATG ACG CCC ATG CCT GTG AAC CAA GCC AAG ACA TAT Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys Thr Tyr 805 810 815	2503
AGA GCA GGT AAA GTA CCA AAT ATG CCC CAA CAG CGA CAA GAC CAA CAT Arg Ala Gly Lys Val Pro Asn Met Pro Gln Gln Arg Gln Asp Gln His 820 825 830	2551
CAT CAA AGC ACC ATG ATG CAC CCA GCC TCC GCG GCA GGG CCA CCC ATC His Gln Ser Thr Met Met His Pro Ala Ser Ala Ala Gly Pro Pro Ile 835 840 845 850	2599
GTA GCC ACC CCG CCC GCT TAC TCC ACT CAG TAC GTT GCC TAC AGC CCT Val Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr Ser Pro 855 860 865	2647
CAG CAG TTT CCC AAT CAG CCT TTG GTC CAG CAT GTG CCG CAT TAT CAG Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His Tyr Gln 870 875 880	2695
TCT CAG CAT CCT CAT GTG TAC AGT CCT GTC ATA CAA GGT AAT GCC AGG Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn Ala Arg 885 890 895	2743
ATG ATG GCA CCA CCA GCA CAT GCT CAG CCT GGT TTA GTG TCT TCT TCA Met Met Ala Pro Pro Ala His Ala Gln Pro Gly Leu Val Ser Ser Ser 900 905 910	2791
GCT GCT CAG TTC GGG GCT CAC GAG CAG ACG CAC GCC ATG TAT GCA TGT Ala Ala Gln Phe Gly Ala His Glu Gln Thr His Ala Met Tyr Ala Cys 915 920 925 930	2839
CCC AAA TTA CCA TAC AAC AAG GAG ACA AGC CCT TCT TTC TAC TTT GCC Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr Phe Ala 935 940 945	2887
ATT TCC ACC GGC TCC CTC GCT CAG CAG TAT GCA CAT CCT AAT GCC GCC Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn Ala Ala 950 955 960	2935
CTG CAT CCA CAT ACT CCC CAT CCT CAG CCT TCG GCC ACT CCC ACC GGA Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly 965 970 975	2983
CAG CAG CAA AGC CAG CAT GGT GGA AGT CAC CCT GCA CCC AGT CCT GTT	3031



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Gln	Gln	Gln	Ser	Gln	His	Gly	Gly	Ser	His	Pro	Ala	Pro	Ser	Pro	Val	
980						985				990						
CAG	CAC	CAT	CAG	CAC	CAG	GCT	GCC	CAG	GCT	CTT	CAT	CTG	GCC	AGT	CCA	3079
Gln	His	His	Gln	His	Gln	Ala	Ala	Gln	Ala	Leu	His	Leu	Ala	Ser	Pro	
995					1000				1005						1010	
CAG	CAG	CAG	TCG	GCC	ATT	TAT	CAT	GCG	GGG	CTG	GCA	CCA	ACA	CCA	CCT	3127
Gln	Gln	Gln	Ser	Ala	Ile	Tyr	His	Ala	Gly	Leu	Ala	Pro	Thr	Pro	Pro	
				1015					1020					1025		
TCC	ATG	ACA	CCT	GCC	TCT	AAT	ACA	CAG	TCT	CCA	CAG	AGC	AGT	TTC	CCA	3175
Ser	Met	Thr	Pro	Ala	Ser	Asn	Thr	Gln	Ser	Pro	Gln	Ser	Ser	Phe	Pro	
			1030					1035					1040			
GCA	GCA	CAA	CAG	ACA	GTC	TTC	ACC	ATC	CAC	CCT	TCT	CAT	GTT	CAG	CCG	3223
Ala	Ala	Gln	Gln	Thr	Val	Phe	Thr	Ile	His	Pro	Ser	His	Val	Gln	Pro	
		1045					1050					1055				
GCA	TAC	ACC	ACC	CCA	CCC	CAC	ATG	GCC	CAC	GTA	CCT	CAG	GCT	CAT	GTA	3271
Ala	Tyr	Thr	Thr	Pro	Pro	His	Met	Ala	His	Val	Pro	Gln	Ala	His	Val	
	1060					1065					1070					
CAG	TCA	GGA	ATG	GTT	CCT	TCT	CAT	CCA	ACT	GCC	CAT	GCG	CCA	ATG	ATG	3319
Gln	Ser	Gly	Met	Val	Pro	Ser	His	Pro	Thr	Ala	His	Ala	Pro	Met	Met	
1075					1080					1085					1090	
CTA	ATG	ACG	ACA	CAG	CCA	CCC	GGT	CCC	AAG	GCC	GCC	CTC	GCT	CAA	AGT	3367
Leu	Met	Thr	Thr	Gln	Pro	Pro	Gly	Pro	Lys	Ala	Ala	Leu	Ala	Gln	Ser	
				1095					1100					1105		
GCA	CTA	CAG	CCC	ATT	CCA	GTT	TCG	ACA	ACA	GCG	CAT	TTC	CCT	TAT	ATG	3415
Ala	Leu	Gln	Pro	Ile	Pro	Val	Ser	Thr	Thr	Ala	His	Phe	Pro	Tyr	Met	
			1110					1115					1120			
ACG	CAC	CCT	TCA	GTA	CAA	GCC	CAC	CAC	CAA	CAG	CAG	TTG	TAA			3457
Thr	His	Pro	Ser	Val	Gln	Ala	His	His	Gln	Gln	Gln	Leu				
		1125					1130					1135				
GGCTGCCTTG	GAGGAACCGA	AAGGCCAAAT	CCCTTCTTCC	CTTCTCTGCT	TCTGCCAACC											3517
GGAAGCACAG	AAAAC TAGAA	CTTCATTGAT	TTTGT TTTT	AAAAGATACA	CTGATTTAAC											3577
ATCTGATAGG	AATGCTAACA	GCTCACTTGC	AGTGGAGGAT	GTTTTGGACC	GAGTAGAGGC											3637
ATGTAGGGAC	TTGTGGCTGT	TCCATAATTC	CATGTGCTGT	TGCAGGGTCC	TGCAAGTACC											3697
CAGCTCTGCT	TGCTGAAACT	GGAAGTTATT	TATTTTTTAA	TGGCCCTTGA	GAGTCATGAA											3757
CACATCAGCT	AGCAACAGAA	GTAACAAGAG	TGATTCTTGC	T												3798

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1135 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Leu Lys Pro<sub>5</sub> Gln Pro Gln Pro<sub>10</sub> Ala Pro Ala Thr Gly Arg<sub>15</sub>  
 Lys Pro Gly Gly<sub>20</sub> Gly Leu Leu Ser<sub>25</sub> Ser Pro Gly Ala Ala Pro Ala Ser<sub>30</sub>  
 Ala Ala Val<sub>35</sub> Thr Ser Ala Ser Val<sub>40</sub> Val Pro Ala Pro<sub>45</sub> Ala Ala Pro Val<sub>50</sub>  
 Ala Ser Ser Ser Ala Ala Ala<sub>55</sub> Gly Gly Gly Arg Pro<sub>60</sub> Gly Leu Gly Arg<sub>65</sub>  
 Gly Arg Asn Ser Ser Lys<sub>70</sub> Gly Leu Pro Gln<sub>75</sub> Pro Thr Ile Ser Phe Asp<sub>80</sub>  
 Gly Ile Tyr Ala Asn<sub>85</sub> Val Arg Met Val His<sub>90</sub> Ile Leu Thr Ser Val<sub>95</sub> Val<sub>100</sub>  
 Gly Ser Lys Cys<sub>100</sub> Glu Val Gln Val Lys<sub>105</sub> Asn Gly Gly Ile Tyr<sub>110</sub> Glu Gly<sub>115</sub>  
 Val Phe Lys Thr Tyr Ser Pro Lys<sub>120</sub> Cys Asp Leu Val Leu<sub>125</sub> Asp Ala Ala<sub>130</sub>  
 His Glu Lys Ser Thr Glu<sub>135</sub> Ser Ser Gly Pro Lys<sub>140</sub> Arg Glu Glu Ile<sub>145</sub>  
 Met Glu Ser Val Leu Phe<sub>150</sub> Lys Cys Ser Asp Phe<sub>155</sub> Val Val Val Gln Phe<sub>160</sub>  
 Lys Asp Thr Asp Ser<sub>165</sub> Ser Tyr Ala Arg Arg<sub>170</sub> Asp Ala Phe Thr Asp<sub>175</sub> Ser<sub>180</sub>  
 Ala Leu Ser Ala<sub>180</sub> Lys Val Asn Gly Glu<sub>185</sub> His Lys Glu Lys Asp<sub>190</sub> Leu Glu<sub>195</sub>  
 Pro Trp Asp<sub>195</sub> Ala Gly Glu Leu Thr<sub>200</sub> Ala Ser Glu Glu Leu<sub>205</sub> Glu Leu Glu<sub>210</sub>  
 Asn Asp Val Ser Asn Gly Trp<sub>215</sub> Asp Pro Asn Asp Met<sub>220</sub> Phe Arg Tyr Asn<sub>225</sub>  
 Glu Glu Asn Tyr Gly Val<sub>230</sub> Val Ser Thr Tyr Asp<sub>235</sub> Ser Ser Leu Ser<sub>240</sub> Ser<sub>245</sub>  
 Tyr Thr Val Pro Leu<sub>245</sub> Glu Arg Asp Asn Ser<sub>250</sub> Glu Glu Phe Leu Lys<sub>255</sub> Arg<sub>260</sub>  
 Glu Ala Arg Ala<sub>260</sub> Asn Gln Leu Ala Glu<sub>265</sub> Glu Ile Glu Ser Ser<sub>270</sub> Ala Gln<sub>275</sub>  
 Tyr Lys Ala Arg Val Ala Leu Glu<sub>280</sub> Asn Asp Asp Arg Ser<sub>285</sub> Glu Glu Glu<sub>290</sub>  
 Lys Tyr Thr Ala Val Gln<sub>295</sub> Arg Asn Cys Ser Asp Arg<sub>300</sub> Glu Gly His Gly<sub>305</sub>  
 Pro Asn Thr Arg Asp Asn<sub>310</sub> Lys Tyr Ile Pro Pro<sub>315</sub> Gly Gln Arg Asn Arg<sub>320</sub>  
 Glu Val Leu Ser Trp Gly Ser Gly Arg Gln Ser Ser Pro Arg Met Gly

325 330 335

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Ala Ser Ala Lys Asp Ser Phe Ile Asp Ser Ser Ser Ser Ser Ser Asn  
660 665 670

Cys Thr Ser Gly Ser Ser Lys Thr Asn Ser Pro Ser Ile Ser Pro Ser  
675 680 685

Met Leu Ser Asn Ala Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln  
690 695 700

Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Arg  
705 710 715 720

Glu Glu Lys Lys Asp Thr Thr Glu Gln Val Arg Lys Ser Thr Leu Asn  
725 730 735

Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro  
740 745 750

Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser  
755 760 765

Met Val Gly His Gln Gln Pro Ala Pro Val Tyr Thr Gln Pro Val Cys  
770 775 780

Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln  
785 790 795 800

Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys  
805 810 815

Thr Tyr Arg Ala Gly Lys Val Pro Asn Met Pro Gln Gln Arg Gln Asp  
820 825 830

Gln His His Gln Ser Thr Met Met His Pro Ala Ser Ala Ala Gly Pro  
835 840 845

Pro Ile Val Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr  
850 855 860

Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His  
865 870 875 880

Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn  
885 890 895

Ala Arg Met Met Ala Pro Pro Ala His Ala Gln Pro Gly Leu Val Ser  
900 905 910

Ser Ser Ala Ala Gln Phe Gly Ala His Glu Gln Thr His Ala Met Tyr  
915 920 925

Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr  
930 935 940

Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn  
945 950 955 960

Ala Ala Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro  
965 970 975

Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser  
980 985 990

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Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala  
995 1000 1005  
Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr  
1010 1015 1020  
Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Ser Ser  
1025 1030 1035 1040  
Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val  
1045 1050 1055  
Gln Pro Ala Tyr Thr Thr Pro Pro His Met Ala His Val Pro Gln Ala  
1060 1065 1070  
His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro  
1075 1080 1085  
Met Met Leu Met Thr Thr Gln Pro Pro Gly Pro Lys Ala Ala Leu Ala  
1090 1095 1100  
Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro  
1105 1110 1115 1120  
Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu  
1125 1130 1135

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGCCCCTCA CCATGTCG

18

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGGCTTGCG GACATTGG

18

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGCGGCTGC CAATGTCC

18

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTAACCGTTC GGCGCCCG

18

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCTCCCGGC GGCTCCTT

18

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCTGCTGCT GCTGGGGCTT CAG

23

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGCCCCGCTC CTCACGTGT

19

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACCCCCGAGA AAGCAACC

18

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCGTTGCCGT TGCTACCA

18

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTCTCATGTG CGGCATCAAG

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 346 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Val Tyr Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Gln Gln Gln Gln
1      5      10      15
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
20     25     30
Gln Pro Pro Pro Ala Ala Ala Asn Val Arg Lys Pro Gly Gly Ser Gly
35     40     45
Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser Pro Ser Ser Ser Val
50     55     60
Ser Ser Ser Ser Ala Thr Ala Pro Ser Ser Val Val Ala Ala Thr Ser
65     70     75     80
Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly Arg Asn Ser Asn Lys Gly
85     90     95
Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly Ile Tyr Ala Asn Met Arg
100    105    110
Met Val His Ile Leu Thr Ser Val Val Gly Ser Lys Cys Glu Val Gln
115    120    125
Val Lys Asn Gly Gly Ile Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro
130    135    140
Lys Cys Asp Leu Val Leu Asp Ala Ala His Glu Lys Ser Thr Glu Ser
145    150    155    160
Ser Ser Gly Pro Lys Arg Glu Glu Ile Met Glu Ser Ile Leu Phe Lys
165    170    175
Cys Ser Asp Phe Val Val Val Gln Phe Lys Asp Met Asp Ser Ser Tyr
180    185    190

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Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala Ile Ser Ala Lys Val Asn  
195 200 205

Gly Glu His Lys Glu Lys Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu  
210 215 220

Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu Asn Asp Val Ser Asn Gly  
225 230 235 240

Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val  
245 250 255

Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu  
260 265 270

Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln  
275 280 285

Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala  
290 295 300

Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln  
305 310 315 320

Arg Asn Ser Ser Glu Arg Glu Gly His Ser Ile Asn Thr Arg Glu Asn  
325 330 335

Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg  
340 345

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 326 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

His Glu Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Pro Gln Pro Pro  
1 5 10 15

Ala Pro Ala Thr Gly Arg Lys Pro Gly Gly Gly Leu Leu Ser Ser Pro  
20 25 30

Gly Ala Ala Pro Ala Ser Ala Ala Val Thr Ser Ala Ser Val Val Pro  
35 40 45

Ala Pro Ala Ala Pro Val Ala Ser Ser Ser Ala Ala Ala Gly Gly Gly  
50 55 60

Arg Pro Gly Leu Gly Arg Gly Arg Asn Ser Ser Lys Gly Leu Pro Gln  
65 70 75 80

Pro Thr Ile Ser Phe Asp Gly Ile Tyr Ala Asn Val Arg Met Val His  
85 90 95

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Ile Leu Thr Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn  
100 105 110  
Gly Gly Ile Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp  
115 120 125  
Leu Val Leu Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly  
130 135 140  
Pro Lys Arg Glu Glu Ile Met Glu Ser Val Leu Phe Lys Cys Ser Asp  
145 150 155 160  
Phe Val Val Val Gln Phe Lys Asp Thr Asp Ser Ser Tyr Ala Arg Arg  
165 170 175  
Asp Ala Phe Thr Asp Ser Ala Leu Ser Ala Lys Val Asn Gly Glu His  
180 185 190  
Lys Glu Lys Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Ser  
195 200 205  
Glu Glu Leu Glu Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn  
210 215 220  
Asp Met Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr  
225 230 235 240  
Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser  
245 250 255  
Glu Glu Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu  
260 265 270  
Ile Glu Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp  
275 280 285  
Asp Arg Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Cys Ser  
290 295 300  
Asp Arg Glu Gly His Gly Pro Asn Thr Arg Asp Asn Lys Tyr Ile Pro  
305 310 315 320  
Pro Gly Gln Arg Asn Arg  
325

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 275 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Ala Pro Gln Pro Pro Pro Pro Gln Gln His Gln Glu Arg Pro Gly  
1 5 10 15

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Ala Ala Ala Ile Gly Ser Ala Arg Gly Gln Ser Thr Gly Lys Gly Pro  
20 25 30  
Pro Gln Ser Pro Val Phe Glu Gly Val Tyr Asn Asn Ser Arg Met Leu  
35 40 45  
His Phe Leu Thr Ala Val Val Gly Ser Thr Cys Asp Val Lys Val Lys  
50 55 60  
Asn Gly Thr Thr Tyr Glu Gly Ile Phe Lys Thr Leu Ser Ser Lys Phe  
65 70 75 80  
Glu Leu Ala Val Asp Ala Val His Arg Lys Ala Ser Glu Pro Ala Gly  
85 90 95  
Gly Pro Arg Arg Glu Asp Ile Val Asp Thr Met Val Phe Lys Pro Ser  
100 105 110  
Asp Val Met Leu Val His Phe Arg Asn Val Asp Phe Asn Tyr Ala Thr  
115 120 125  
Lys Asp Lys Phe Thr Asp Ser Ala Ile Ala Met Asn Ser Lys Val Asn  
130 135 140  
Gly Glu His Lys Glu Lys Val Leu Gln Arg Trp Glu Gly Gly Asp Ser  
145 150 155 160  
Asn Ser Asp Asp Tyr Asp Leu Glu Ser Asp Met Ser Asn Gly Trp Asp  
165 170 175  
Pro Asn Glu Met Phe Lys Phe Asn Glu Glu Asn Tyr Gly Val Lys Thr  
180 185 190  
Thr Tyr Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Lys Asp  
195 200 205  
Asn Ser Glu Glu Phe Arg Gln Arg Glu Leu Arg Ala Ala Gln Leu Ala  
210 215 220  
Arg Glu Ile Glu Ser Ser Pro Gln Tyr Arg Leu Arg Ile Ala Met Glu  
225 230 235 240  
Asn Asp Asp Gly Arg Thr Glu Glu Glu Lys His Ser Ala Val Gln Arg  
245 250 255  
Gln Gly Ser Gly Arg Glu Ser Pro Ser Leu Ala Ser Arg Glu Gly Lys  
260 265 270  
Tyr Ile Pro  
275

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1257 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..1255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

G CAC GAG GGG CCG CTC ACC ATG TCG CTG AAG CCG CAG CCG CAG CCG	46
His Glu Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Pro Gln Pro	15
1 5 10	
CCC GCG CCC GCC ACT GGC CGC AAG CCC GGC GGC GGC CTG CTC TCG TCG	94
Pro Ala Pro Ala Thr Gly Arg Lys Pro Gly Gly Gly Leu Leu Ser Ser	30
20 25	
CCC GGC GCC GCG CCG GCC TCG GCC GCG GTG ACC TCG GCT TCC GTG GTG	142
Pro Gly Ala Ala Pro Ala Ser Ala Ala Val Thr Ser Ala Ser Val Val	45
35 40	
CCG GCC CCG GCC GCG CCG GTG GCG TCT TCC TCG GCG GCC GCG GGC GGC	190
Pro Ala Pro Ala Ala Pro Val Ala Ser Ser Ser Ala Ala Ala Gly Gly	60
50 55	
GGG CGT CCC GGC CTG GGC AGA GGT CGG AAC AGT AGC AAA GGA CTG CCT	238
Gly Arg Pro Gly Leu Gly Arg Gly Arg Asn Ser Ser Lys Gly Leu Pro	75
65 70	
CAG CCT ACG ATT TCT TTT GAT GGA ATC TAT GCA AAC GTG AGG ATG GTT	286
Gln Pro Thr Ile Ser Phe Asp Gly Ile Tyr Ala Asn Val Arg Met Val	95
80 85 90	
CAT ATA CTT ACG TCA GTT GTT GGA TCG AAA TGT GAA GTA CAA GTG AAA	334
His Ile Leu Thr Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys	110
100 105	
AAC GGA GGC ATA TAT GAA GGA GTT TTT AAA ACA TAC AGT CCT AAG TGT	382
Asn Gly Gly Ile Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys	125
115 120	
GAC TTG GTA CTT GAT GCT GCA CAT GAG AAA AGT ACA GAA TCC AGT TCG	430
Asp Leu Val Leu Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser	140
130 135	
GGG CCA AAA CGT GAA GAA ATA ATG GAG AGT GTT TTG TTC AAA TGC TCA	478
Gly Pro Lys Arg Glu Glu Ile Met Glu Ser Val Leu Phe Lys Cys Ser	155
145 150	
GAC TTC GTT GTG GTA CAG TTT AAA GAT ACA GAC TCC AGT TAT GCA CGG	526
Asp Phe Val Val Val Gln Phe Lys Asp Thr Asp Ser Ser Tyr Ala Arg	175
160 165 170	
AGA GAT GCT TTT ACT GAC TCT GCT CTC AGC GCA AAG GTG AAT GGT GAG	574
Arg Asp Ala Phe Thr Asp Ser Ala Leu Ser Ala Lys Val Asn Gly Glu	190
180 185	
CAC AAG GAG AAG GAC CTG GAG CCC TGG GAT GCA GGG GAG CTC ACG GCC	622
His Lys Glu Lys Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala	205
195 200	
AGC GAG GAG CTG GAG CTG GAG AAT GAT GTG TCT AAT GGA TGG GAC CCC	670
Ser Glu Glu Leu Glu Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro	220
210 215 220	

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AAT GAC ATG TTT CGA TAT AAT GAA GAG AAT TAT GGT GTG GTG TCC ACA Asn Asp Met Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr 225 230 235	718
TAT GAT AGC AGT TTA TCT TCA TAT ACG GTT CCT TTA GAA AGG GAC AAC Tyr Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn 240 245 250 255	766
TCA GAA GAA TTT CTT AAA CGG GAG GCA AGG GCA AAC CAG TTA GCA GAA Ser Glu Glu Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu 260 265 270	814
GAA ATT GAA TCC AGT GCT CAG TAC AAA GCT CGT GTC GCC CTT GAG AAT Glu Ile Glu Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn 275 280 285	862
GAT GAC CGG AGT GAG GAA GAA AAA TAC ACA GCA GTC CAG AGA AAC TGC Asp Asp Arg Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Cys 290 295 300	910
AGT GAC CGG GAG GGG CAT GGC CCC AAC ACT AGG GAC AAT AAA TAT ATT Ser Asp Arg Glu Gly His Gly Pro Asn Thr Arg Asp Asn Lys Tyr Ile 305 310 315	958
CCT CCT GGA CAA AGA AAC AGA GAA GTC CTA TCC TGG GGA AGT GGG AGA Pro Pro Gly Gln Arg Asn Arg Glu Val Leu Ser Trp Gly Ser Gly Arg 320 325 330 335	1006
CAG AGC TCA CCA CGG ATG GGC CAG CCT GGG CCA GGC TCC ATG CCG TCA Gln Ser Ser Pro Arg Met Gly Gln Pro Gly Pro Gly Ser Met Pro Ser 340 345 350	1054
AGA GCT GCT TCT CAC ACT TCA GAT TTC AAC CCG AAC GCT GGC TCA GAC Arg Ala Ala Ser His Thr Ser Asp Phe Asn Pro Asn Ala Gly Ser Asp 355 360 365	1102
CAA AGA GTA GTT AAT GGA GGT GTT CCC TGG CCA TCG CCT TGC CCA TCT Gln Arg Val Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser 370 375 380	1150
CCT TCC TCT CGC CCA CCT TCT CGC TAC CAG TCA GGT CCC AAC TCT CTT Pro Ser Ser Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu 385 390 395	1198
CCA CCT CGG GCA GCC ACC CCT ACA CGG CCT CGT GCC GAA TTC CTG CAG Pro Pro Arg Ala Ala Thr Pro Thr Arg Pro Arg Ala Glu Phe Leu Gln 400 405 410 415	1246
CCC GGG GAT CC Pro Gly Asp	1257